

SEQUENCE LISTING

5 <110> Larsen, Christian P.
 Pearson, Thomas C.
 Waller, Edmund K.
 Adams, Andrew B.

10 <120> METHODS OF INDUCING ORGAN TRANSPLANT TOLERANCE AND
 CORRECTING HEMOGLOBINOPATHIES

<130> D0136NP/30436.58USU1

15 <140> Not yet known
 <141> 2002-01-25

<150> 60/264,528
 <151> 2001-01-26

20 <150> 60/303,142
 <151> 2001-07-05

<160> 20

25 <170> PatentIn Ver. 2.1

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 <213> Artificial Sequence

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 ggcacgcta gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180
 acagtgtctt ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
 40 gggaatgagt tgaccttctt agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
 gagctcatgt acccaccgcc atactacgag ggcataaggca acggaaccca gatttatgta 420
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 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720
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 55 ccgggtaaat ga 1152

<210> 2
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 <212> PRT
 <213> Artificial Sequence

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<220>
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 sequence

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 Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1 5 10 15

15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30

Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45

20

Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60

Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75 80

25

Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
 85 90 95

30

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
 100 105 110

Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
 115 120 125

35

Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
 130 135 140

Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
 145 150 155 160

40

Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
 165 170 175

45

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 180 185 190

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 195 200 205

50

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 210 215 220

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 225 230 235 240

55

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 245 250 255

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Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
      260              265              270

5  Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
      275              280              285

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
      290              295              300

10 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
      305              310              315              320

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
      325              330              335

15 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
      340              345              350

20 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
      355              360              365

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
      370              375              380

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30  <213> Artificial Sequence

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40  acagtgtctt gccagggctga cagccagggt actgaagtct gtgcggcaac ctacatgatg 240
    gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
    gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggt 360
    gagctcatgt acccaccgcc atactacgag ggcataggca acggaaccca gatttatgta 420
    attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
45  acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540
    ccaaaaccca aggacacct catgatctcc cggacccctg aggtcacatg cgtgggtggtg 600
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    cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720
    gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caagggtctc 780
50  aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
    gaaccacagg tgtacacct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
    ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
    gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020
    ttctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1080
55  tgctccgtga tgcattgagg tctgcacaac cactacacgc agaagagcct ctccctgtct 1140
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                                     1152

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<210> 4
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 <212> PRT
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<220>
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 1 5 10 15

15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30

Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45

20

Tyr Ala Ser Pro Gly Lys Tyr Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60

25

Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75 80

Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
 85 90 95

30

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
 100 105 110

Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
 115 120 125

35

Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
 130 135 140

40

Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
 145 150 155 160

Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
 165 170 175

45

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 180 185 190

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 195 200 205

50

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 210 215 220

55

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 225 230 235 240

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys

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	Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile		
	260	265	270
5	Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro		
	275	280	285
10	Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu		
	290	295	300
	Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn		
	305	310	315 320
15	Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser		
	325	330	335
	Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg		
	340	345	350
20	Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu		
	355	360	365
	His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
25	370	375	380
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45	attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480		
	acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540		
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	cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtgggtcagc 720		
50	gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caagggtctcc 780		
	aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840		
	gaaccacagg tgtacacctt gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900		
	ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960		
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	tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1140		
	ccgggtaaat ga		1152

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
245 250 255

5 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
260 265 270

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
275 280 285

10 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
290 295 300

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
305 310 315 320

15 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
325 330 335

20 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
340 345 350

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
355 360 365

25 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375 380

30 <210> 7
<211> 1152
<212> DNA
<213> Artificial Sequence

35 <220>
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50 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg lgtgggtcagc 720
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55 gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020
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1152

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<212> PRT
<213> Artificial Sequence

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Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
25 35 40 45
Tyr Ala Ser Pro Gly Lys Thr Thr Glu Val Arg Val Thr Val Leu Arg
50 55 60
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65 70 75 80
Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
30 85 90 95
Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100 105 110
Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
35 115 120 125
Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140
Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
40 145 150 155 160
Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
45 165 170 175
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
180 185 190
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
50 195 200 205
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
210 215 220
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
55 225 230 235 240

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Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
245 250 255

5 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
260 265 270

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
275 280 285

10 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
290 295 300

15 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
305 310 315 320

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
325 330 335

20 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
340 345 350

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
355 360 365

25 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375 380

30 <210> 9
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<212> DNA
<213> Artificial Sequence

35 <220>
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gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
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<212> PRT
<213> Artificial Sequence

10 <220>
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20 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35 40 45

25 Tyr Ala Ser Pro Gly Lys Trp Thr Glu Val Arg Val Thr Val Leu Arg
50 55 60

Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65 70 75 80

30 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
85 90 95

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100 105 110

35 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
115 120 125

40 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140

Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
145 150 155 160

45 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
165 170 175

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
180 185 190

50 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
195 200 205

55 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
210 215 220

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser

	225		230		235		240									
	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
				245						250					255	
5	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile
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10	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
			275					280					285			
	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu
		290					295					300				
15	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	305					310					315					320
	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
					325					330					335	
20	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg
				340					345					350		
	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
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Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
      50              55              60

10 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
      65              70              75              80

Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
15      85              90              95

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
      100             105             110

20 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
      115             120             125

Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
      130             135             140

25 Pro Cys Pro Asp Ser Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser
      145             150             155             160

Ser Gly Leu Phe Phe Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser
30      165             170             175

Lys Met Leu Lys Lys Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys
      180             185             190

35 Met Pro Pro Thr Glu Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe
      195             200             205

Ile Pro Ile Asn
      210

40 <210> 13
    <211> 1152
    <212> DNA
    <213> Artificial Sequence

45 <220>
    <223> Description of Artificial Sequence: CTLA4Ig
        sequence

50 <400> 13
    atgggtgtac tgctcacaca gaggacgctg ctcagtctgg tccttgcaact cctgtttcca 60
    agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggtagctggc cagcagccga 120
    ggcacgcta gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180
55 acagtgcctc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
    gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
    gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360

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gagctcatgt acccaccgcc atactacctg ggcataaggca acggaaccca gatttatgta 420
attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
acatccccac cgtccccagc acctgaactc ctgggtggat cgtcagctt cctcttcccc 540
ccaaaacca aggacaccct catgatctcc cggaccctg aggtcacatg cgtggtggtg 600
5 gagtgagcc acgaagacc tgaggtcaag ttcaactggt acgtggacgg cgtggagggtg 660
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg ggtggtcagc 720
gtcctcaccg tctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
gaaccacagg tgtacacct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
10 ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020
ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1080
tgctccgtga tgcattgagg tctgcacaac cactacacgc agaagagcct ctccctgtct 1140
ccgggtaaat ga 1152

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15

<210> 14

<211> 383

<212> PRT

20

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CTLA4Ig
sequence

25

<400> 14

Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1 5 10 15

30

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
20 25 30

Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35 40 45

35

Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
50 55 60

40

Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65 70 75 80

Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
85 90 95

45

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100 105 110

Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
115 120 125

50

Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140

55

Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
145 150 155 160

Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val

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	165	170	175
	Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr		
5	180	185	190
	Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu		
	195	200	205
10	Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys		
	210	215	220
	Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser		
	225	230	235 240
15	Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys		
	245	250	255
	Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile		
20	260	265	270
	Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro		
	275	280	285
25	Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu		
	290	295	300
	Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn		
	305	310	315 320
30	Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser		
	325	330	335
	Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg		
35	340	345	350
	Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu		
	355	360	365
40	His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
	370	375	380
45	<210> 15		
	<211> 6		
	<212> PRT		
	<213> Homo sapiens		
50	<400> 15		
	Met Tyr Pro Pro Pro Tyr		
	1	5	
55	<210> 16		
	<211> 65		
	<212> DNA		
	<213> Artificial Sequence		

<220>
<223> Description of Artificial Sequence: primer
sequence encoding Oncostatin M-CTLA4 fusion

5 <400> 16
ctcagtctgg tccttgcaact cctgtttcca agcatggcga gcatggcaat gcacgtggcc 60
cagcc 65

10 <210> 17
<211> 33
<212> DNA
<213> Artificial Sequence

15 <220>
<223> Description of Artificial Sequence: primer
sequence encoding CTLA4 sequence

20 <400> 17
tttgggctcc tgatcagaat ctgggcacgg ttg 33

25 <210> 18
<211> 72
<212> DNA
<213> Artificial Sequence

30 <220>
<223> Description of Artificial Sequence: primer
sequence encoding Oncostatin M signal peptide
sequence

35 <400> 18
ctagccactg aagcttcacc aatgggtgta ctgctcacac agaggacgct gctcagtctg 60
gtccttgcaac tc 72

40 <210> 19
<211> 41
<212> DNA
<213> Artificial Sequence

45 <220>
<223> Description of Artificial Sequence: primer
sequence from vector sequence

<400> 19
gaggtgataa agcttcacca atgggtgtac tgctcacaca g 41

50 <210> 20
<211> 42
<212> DNA
<213> Artificial Sequence

55 <220>
<223> Description of Artificial Sequence: primer

sequence encoding CTLA4 sequence

<400> 20

gtggtgtatt ggtctagatc aatcagaatc tgggcacggt tc

42

5

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